

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/572,027BDATE: 05/06/98
TIME: 12:59:02

INPUT SET: S25565.raw

This Raw Listing contains the General
Information Section and up to the first 6 pages

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: DeBonte, L. et al.

(ii) TITLE OF INVENTION: PLANTS HAVING MUTANT SEQUENCES THAT CONFER
ALTERED FATTY ACID PROFILES

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fish & Richardson P.C., P.A.
(B) STREET: 60 South Sixth Street, Suite 3300
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: USA
(F) ZIP: 55402

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM compatible
(C) OPERATING SYSTEM: Windows95
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/572,027
(B) FILING DATE: 14-DEC-1995
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/416,497
(B) FILING DATE: 04-APR-1995
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/170,886
(B) FILING DATE: 21-DEC-1993
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/739,965
(B) FILING DATE: 05-AUG-1991
(C) CLASSIFICATION:

RECEIVED

DEC 02 1998

Publishing Division
Corres/Allowed Files (09)

RAW SEQUENCE LISTING PATENT APPLICATION US/08/572,027B

DATE: 05/06/98
TIME: 12:59:03

INPUT SET: S25565.raw

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47      (vi) PRIOR APPLICATION DATA:
48          (A) APPLICATION NUMBER: US 07/575,542
49          (B) FILING DATE: 30-AUG-1990
50          (C) CLASSIFICATION:
51
52      (viii) ATTORNEY/AGENT INFORMATION:
53          (A) NAME: Ellinger, Mark S.
54          (B) REGISTRATION NUMBER: 34,812
55          (C) REFERENCE/DOCKET NUMBER: A21-535.10
56
57      (ix) TELECOMMUNICATION INFORMATION:
58          (A) TELEPHONE: 612/335-5070
59          (B) TELEFAX: 612/288-9696
60
61      (2) INFORMATION FOR SEQ ID NO:1:
62
63          (i) SEQUENCE CHARACTERISTICS:
64              (A) LENGTH: 1155 base pairs
65              (B) TYPE: nucleic acid
66              (C) STRANDEDNESS: single
67              (D) TOPOLOGY: linear
68
69          (ii) MOLECULE TYPE: DNA
70
71          (iii) HYPOTHETICAL: NO
72
73          (iv) ANTI-SENSE: NO
74
75          (vi) ORIGINAL SOURCE:
76              (A) ORGANISM: Brassica napus
77
78          (ix) FEATURE:
79              (D) OTHER INFORMATION: Wild type F form.
80
81
82          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
83
84      ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT      48
85      Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
86          1              5              10              15
87
88      GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT      96
89      Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
90          20              25              30
91
92      GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG      144
93      Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
94          35              40              45
95
96      ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC      192
97      Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
98          50              55              60
99

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/572,027B

DATE: 05/06/98
TIME: 12:59:04

INPUT SET: S25565.raw

100	TGC	TTC	TAC	TAC	NTC	GCC	ACC	ACT	TAC	TTC	CCT	CTC	CTC	CCT	CAC	CCT	240
101	Cys	Phe	Tyr	Tyr	Xaa	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro	
102	65					70					75					80	
103																	
104	CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAA	GGG	TGC	GTC	288
105	Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	
106					85					90					95		
107																	
108	CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	GAA	TGC	GGC	CAC	CAC	GCC	TTC	336
109	Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe	
110				100					105					110			
111																	
112	AGC	GAC	TAC	CAG	TGG	CTT	GAC	GAC	ACC	GTC	GGT	CTC	ATC	TTC	CAC	TCC	384
113	Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser	
114			115					120					125				
115																	
116	TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGC	AGC	CAC	432
117	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Ser	His	
118		130					135					140					
119																	
120	CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG	480
121	His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	
122	145					150				155						160	
123	AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGC	AAG	TAC	CTC	AAC	AAC	CCT	TTG	528
124	Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	
125				165					170					175			
126																	
127	GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG	TTC	ACT	CTC	GGC	TGG	CCG	TTG	576
128	Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu	
129				180					185				190				
130																	
131	TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGA	AGA	CCT	TAC	GAC	GGC	GGC	TTC	CGT	624
132	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg	
133			195					200					205				
134																	
135	TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGC	GAG	CGT	CTC	672
136	Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	
137		210					215					220					
138																	
139	CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	TAC	GGT	CTC	720
140	Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu	
141	225					230					235					240	
142																	
143	TTC	CGT	TAC	GCC	GCC	GGC	CAG	GGA	GTG	GCC	TCG	ATG	GTC	TGC	TTC	TAC	768
144	Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr	
145				245						250					255		
146																	
147	GGA	GTC	CCG	CTT	CTG	ATT	GTC	AAT	GGT	TTC	CTC	GTG	TTG	ATC	ACT	TAC	816
148	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr	
149				260					265					270			
150																	
151	TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT	CAC	TAC	GAT	TCG	TCC	GAG	TGG	864
152	Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/572,027B

DATE: 05/06/98
TIME: 12:59:05

INPUT SET: S25565.raw

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153          275          280          285
154
155  GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC      912
156  Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
157      290          295          300
158
159  TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT      960
160  Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
161  305          310          315          320
162
163  CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG      1008
164  Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
165      325          330          335
166
167  ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG      1056
168  Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
169      340          345          350
170
171  GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG      1104
172  Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
173      355          360          365
174
175  GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T      1153
176  Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
177      370          375          380
178
179  GA      1155
180
181
182  (2) INFORMATION FOR SEQ ID NO:2:
183
184      (i) SEQUENCE CHARACTERISTICS:
185          (A) LENGTH: 384 amino acids
186          (B) TYPE: amino acid
187          (D) TOPOLOGY: linear
188
189      (ii) MOLECULE TYPE: protein
190
191      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
192
193  Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
194      1          5          10          15
195
196  Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
197      20          25          30
198
199  Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
200      35          40          45
201
202  Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
203      50          55          60
204
205  Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/572,027B

DATE: 05/06/98
TIME: 12:59:06

INPUT SET: S25565.raw

	65	70	75	80
206				
207				
208	Leu Ser Tyr Phe	Ala Trp Pro Leu Tyr Trp	Ala Cys Gln Gly Cys Val	
209		85	90	95
210				
211	Leu Thr Gly Val	Trp Val Ile Ala His Glu Cys Gly His His Ala Phe		
212		100	105	110
213				
214	Ser Asp Tyr Gln	Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser		
215		115	120	125
216				
217	Phe Leu Leu Val	Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His		
218		130	135	140
219				
220	His Ser Asn Thr	Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys		
221		145	150	155
222				
223	Lys Lys Ser Asp	Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu		
224		165	170	175
225				
226	Gly Arg Thr Val	Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu		
227		180	185	190
228				
229	Tyr Leu Ala Phe	Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg		
230		195	200	205
231				
232	Cys His Phe His	Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu		
233		210	215	220
234				
235	Gln Ile Tyr Ile	Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu		
236		225	230	235
237				
238	Phe Arg Tyr Ala	Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr		
239		245	250	255
240				
241	Gly Val Pro Leu	Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr		
242		260	265	270
243				
244	Leu Gln His Thr	His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp		
245		275	280	285
246				
247	Asp Trp Phe Arg	Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile		
248		290	295	300
249				
250	Leu Asn Lys Val	Phe His Asn Ile Thr Asp Thr His Val Ala His His		
251		305	310	315
252				
253	Pro Phe Ser Thr	Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala		
254		325	330	335
255				
256	Ile Lys Pro Ile	Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val		
257		340	345	350
258				

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/572,027B

DATE: 05/06/98
TIME: 12:59:07

INPUT SET: S25565.raw

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Original Text